

; Sequence 12, Application US/10030203  
; GENERAL INFORMATION:  
; APPLICANT: Alán Garen  
; APPLICANT: Zhiwei Hu  
; TITLE OF INVENTION: Neovascular-Targeted Immunoconjugates

; FILE REFERENCE: OCR-679B.US  
; CURRENT APPLICATION NUMBER: US/10/030,203  
; CURRENT FILING DATE: 2001-12-31  
; PRIOR APPLICATION NUMBER: PCT/US00/16481  
; PRIOR FILING DATE: 2000-06-14  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: MS DOS

; SEQ ID NO 12

; LENGTH: 2138

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: CDS

; OTHER INFORMATION: hfvliasm immunoconjugate

; OTHER INFORMATION: includes leader + hfvliasm + human IgG1FC

US-10-030-203-12-11

KLCRDFIMVSOALRLGLLGLGQCLAAGVAKASGETRDMPKPGHVRVFTOEAHGVLRHRRANA  
FLEELRPGSLRECEKBOCSPEAREIKDAERTKLFWISYSDGQACSSPCONGSKCKDQLOSYICFL  
PAFEGNRCEHTKDDQICWENGGCEQYCSHTGTRKCRCHGSLLDAGSVCTVEYPCGKIPILEK  
RNASKPQRI VGGKVPKGECEBQVLLLVNGAQLCGGLTINTIWWVSAACHFDKIKNRNLLIAGEHDL  
SEHDDEQSRRAVQIIPSTVYVGTTHDIALRLHQPVLTDHVVPLCLPERTFERTLAFVRFSLVSG  
WGQLLDRGATALELAVLNPRLTQDCLQOSKRVGDSNITREYFCAGYSDGSKDCAGDSGGPHATYR  
GTWYLTGVWGOGCATVGHFGVTVRSQYIEWLOKLMREBPRPGVLLRAAPPFGSAEPKSCDKHTCCPC  
PAPELLGSPVFLFPKPKOTLMIISRTBEVTCVVDVSHEDDEVXFNVDGVEVHAKTKREEQYNST  
YRVVSVLTVHQDLWNGKEYCKCKNSKALPAPIEKTIKAKQGPXEQVYITLPPSRDELTKNQVSLTCLV  
KGFPSDIAVWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSRWQQGNVFCVNMHEALHNHYTQK  
SLSLSGPGKXXAAI

US-10-030-203-12-2

SFAEISSWSPPRSGSSAFCFLFRAAWLQAGSLRPOEEKHCTCRSGRLTSSXPRKPTASCTGAGATPR  
SWRSCGRAPWRGSRARSAPSRRRSGSTRRGRCSGLTVMGTSVPOVHARMGAPARTSSSPISASAS  
LPSSATVTRMTSTXSVKTAATVSTTAFTAPASVAGTATGTCQTPAHPOLNIHVEKYLFXK  
EMPNAPKAEIAGCAPKSGHSCCWMKELSCVGGXSTPSGMSPRPTVSTKSTGTGTXSCWASTTS  
ASTGMSRAGWRRSSSPARTPTTTRCSACTSPWSLSLTMWCPACPNRSLRGWRWPCASHWSAA  
GASCVTAPRWSXCTCGXXPTACSHGRETPOISRSTCSVPATMAARTPARCTVEAHMPPPTTG  
ARGTXRASSAGAAQWATLCTGTPSPSTSGCKSSCAQSHAQSSCEPHFPDQPSNLVTKLTHARRA  
QHLNSWGRQSSSQNPRTPTPSXPGPLURSHAWMTXATILURSSSTGTWTAWRCIXPRQSRGRSSTAR  
TWSSSPSCTRTGMARSTARSPTKSPSPSRKPSKPGKSPENXCTCPCPHGMSXPRTSRXAPAWS  
KASIPATSPWSGRAMSRRTTTRPRLPCWPTTAPSSSTASSPWTBAGGSRGTSSHAPXCMRLCTTTTTRR  
ASPLRVNDKRP1

US-10-030-203-12-3

ALQRPHGLPGQAPFLPNAWASGLPGCRRGRXGLRRNTGHAVEAGASOSLUNPGSPRRPAPAPARQV  
PGAAAGLPGEVQGVALLRGPGDLOQGRDEDAVLDFLOXWGPVCLSKMPEWLLQGPAPVLYLLLP  
CLRGPELDAQCPADLCERERRLXAVLQXPHGQALLSVPRGVLISAGRGVLHTHSXIISMWKNTYRKK  
KCOOTPRNCGGQVPGQGVGWSVGVWGDPDQHLGLGRLPFRQNOLEBPDGRAGRARPO  
RARRCXAPAGAGHHPHVRPGHOPHRAAPAPARGPHXPCGAPLPARTDVLKEDAGLRALLIGORL  
GPAAGPWRHGPAGHCAQAPADDPGLPAAVTEGGRLPKYGHVHVCRLLCWOQGLLRGCQWRPTCHPLPG  
HVVPDGHQOLGGLNRNGLMGVHQGLPVRHVAKAHALRATPRSPAPSPISIRRAQILIXQNSHMTVP  
STXTPGGTVSLPLPKTKQGHDPDPXGMRGGRREPRRGXQVQLVGRGEGXACQDKAAGGAVQOHV  
PCQRPHRPAPGLAEWQGVQVQLOQSPSPHRENHLOSQRAAPRTTGVHPAPIPGXADQEPGQDLPQV  
RLLSQRHRRGVGEQWAAEQLOQHASRAGLRLLLPLOQAHRGQEQVAAGERLLMLRDXAGSAQPLHAE  
PLPVSGXMTSG1

US-10-030-203-12-4

AAAYHLPGDRERLFCVXMLCRASCITEHEKTPCCCHLLSTVLSLXKRKEPSESSTGGVVLXLFSGCPLL  
SWRTAMSLCKXPLTKQVRLTWPLVSSRRDGRVYTCXSGCPALAMFVSMGAGRALLFTLHLYSPFGK  
SWCRTVRLTTRYVLLYCSRRGFVLAICTSTSTYQNLNTSGSSWLTTSTHTVTSREIMRVSLGFGK  
RKTDPGPRSSGAGHGHVXVLSQDLSADPGNARRTPGRGSRMFCSSHMYETLVYTPKMTVAQP  
WQOLTWPVRYHVPXWACCPPLSPAQESLLISEXPAQNMYSVIFGESPTFRDCCQSWISRGTLSTWS  
SRAPAPRSSSPQPLTNEKRTKLSVLSNVRSGRGTITWVRTTCWCRRSRSMGMLVVPVTYVILGMMTC  
ATRLCLSPSCSLRSCSPSTAIRFLQFLSKQAAETQMVLIRVPHNXAPFTNNRTCHGHSPLGHTL  
PTTIRPWGLLAFLSRIGIFPHGYSTVGQDTPSWAREYPSWHRQERLVPVMSLOYQSPSPFTQISWS  
SLCVSQRPSPKAGROKOIXDWSWSLQEPPEPHGLAHWSPSLXIQNSFVLSASLKI SRASSKEHCSSLH  
SLSRFPGRSSSNALARRRRCRTPWASSWVTYTLXGPGFHGMSVSPPEALATPPAARQPSXPSRRQRSL  
RAWETMKSLSQ1

US-10-030-203-12-5

RPLIIPETGRSSACSCABPHASRRMRRSPATCSPXACCRRRRRSPAREAWSCSCSPAHCS  
PTPRCRWDRSLXPGRSXGPGSWAHGPGWAGCTPVLGAALMLWRWFRWGLGLCWRCCTCTCHSAS  
PGAGRXGRPHGTCCCTTAPPAALSWYAPRRRPTSTXPOGLRGRSPPRMXPOGSGRSXGCPWVLGR  
GRLTVPCGVQVLGTVMCFECHKIWALRI REMGLAGLLGVALSAXAFATCTCTGRPWCCTPOSGPRLRSP  
GPSXRCPSGTTTCCPSGWHVHLCPRRSPCCCHPSRHRHTCTPYLGLSLPPSVTAAGSPGSSAGAXAXA  
PGPMHGAAGSPSRMRSARRPASSQRTSVRAGRGAPHQXQPRAGAGAAACRGWCPGRTCMGXFXPA  
PPAGSAHPRARXGRARPAFRSGSSSFCRNSGPRRPRMCKSPGHTTELHSTPTGAMDTPLWGTFC  
PPQGLGVCHWHFFLEXYFHMDIQLMWYCRTPRLPAESTPRGTRDSAWCPCGCHCTAHSRRSRHSAGH  
PCASHSGPRQGGRSRYRTGAGPCRPCSPHSGMDLRHTGPHCKRKTASSSPRXPSPGPPRRSTAPCT  
PSGSPAAAPCTGTRWRAGAGARRGLPGLRLCEAPASTACTCVFLLLRPRXRLPQSPSEAQAEGRGAX  
GPGRFXNLXAI

US-10-030-203-12-6

GRLSFTRRQGEALLRVVVVQSLMHHGAXEDVPLLPALVHGELAVEBEGAVGVQHRRGLVVVLRPLIAL  
PLHGDVAGIEAFDQAGQADLVLGQLIPGMGQCVHLXFGSLPFGDGLDGWEGFVGDALVLALIQV  
LVQDGEDADHTVRAVVLRLPRLCLGXMHLLHAVHVPVELDLRVFAVHHHACDLRGPDGHEGVLGWGE  
EDXSPOEFRCWAWACYSVFVTRFGLCGSGKWSQEDSWMLXAHELLQPLDVLGDGPGVHPKVAHGCAAL  
APADDARQVPRAPVVGGMWASTVPRAGVLAALIRVAGTEHLVDIMGVSHLPLXLLQAVLGHQGHVEHEL  
QGRGATVQOLAPAADQXEAHEGQRPRLBRPFGAEGHMSVEDHGLVQAEQKDVVVGGLDVRAGDDDLR  
HPPALLIPVLAEVVLAQHRDQVPPVLDVETVGRGDHPDGVDDQGPPTQLSSIHOQODLPMTLPLFGAHLI  
PHNSALGFAGISFFXNRYFSTWIFNCGCAGHPVCCQRPVLPVAPTALGARVVTVALLTAALVHTDQLVI  
LVRLTVPALEGREAEADIGLELVLGAPILAWTQGLVPIITVRNPEQLRPLRVLEDLPGLLEGALLLLAL  
PLOGARPOLLQERVGAAPVQDAVGLFLGYEDSVRPLRPHVPCFSSXGLSDPACSAQALKPKQAEPEE  
GLGDHDEISAKI

**This Page Blank (uspto)**

> O < IntelliGenetics  
> O <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file us-10-617-619-7.res made by Jdelaval on Tue 15 Feb 105 11:34:06-PST.

Query sequence being compared: US-10-617-619-7 (1-232)

Number of sequences searched: 6

Number of scores above cutoff: 6

Results of the initial comparison of US-10-617-619-7 (1-232) with:  
File : trans.pep

100-										
N	-	-	-	-	-	-	-	-	-	-
U	50-	-	-	-	-	-	-	-	-	-
M	-	-	-	-	-	-	-	-	-	-
B	-	-	-	-	-	-	-	-	-	-
E	-	-	-	-	-	-	-	-	-	-
R	-	-	-	-	-	-	-	-	-	-
O	-	-	-	-	-	-	-	-	-	-
F	10-	-	-	-	-	-	-	-	-	-
S	-	-	-	-	-	-	-	-	-	-
E	5-	-	-	-	-	-	-	-	-	-
Q	-	-	-	-	-	-	-	-	-	-
U	-	-	-	-	-	-	-	-	-	-
E	-	-	-	-	-	-	-	-	-	-
N	-	-	-	-	-	-	-	-	-	-
C	-	-	-	-	-	-	-	-	-	-
E	-	-	-	-	-	-	-	-	-	-
S	0	-	-	-	-	-	-	-	-	-
SCORE	0	26	51	77	102	128	153	179	204	230
STDEV					1				2	

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	32
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	43	6	91.61
Times:	CPU	Total Elapsed	
	00:00:00.00	00:00:00.00	

Number of residues: 4270  
Number of sequences searched: 6  
Number of scores above cutoff: 6

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Sig.	Frame	Init.	Opt.
-----							
**** 2 standard deviations above mean ****							
1. US-10-030-203-12	Sequence 12, Application US/10030203	712	230	2.04	0		
**** 0 standard deviation from mean ****							
2. US-10-030-203-12		711	7	34	-0.39	0	
3. US-10-030-203-12		712	6	32	-0.40	0	
4. US-10-030-203-12		711	5	7	-0.41	0	
5. US-10-030-203-12		712	5	37	-0.41	0	
6. US-10-030-203-12		712	5	40	-0.41	0	
-----							
1. US-10-617-619-7 (1-232)							
-----							
Sequence 12, Application US/10030203							
GENERAL INFORMATION:							
APPLICANT: Alan Garen							
APPLICANT: Zhiwei Hu							
TITLE OF INVENTION: Neovascular-Targeted Immunoconjugates							
FILE REFERENCE: OCR-679B.US							
CURRENT APPLICATION NUMBER: US/10/030,203							
CURRENT FILING DATE: 2001-12-31							
PRIOR APPLICATION NUMBER: PCT/US00/16481							
PRIOR FILING DATE: 2000-06-14							
NUMBER OF SEQ ID NOS: 12							
SOFTWARE: MS DOS							
SEQ ID NO 12							
LENGTH: 2138							
TYPE: DNA							
ORGANISM: Artificial Sequence							
FEATURE:							
NAME/KEY: CDS							
OTHER INFORMATION: hfVilasm immunoconjugate							
OTHER INFORMATION: includes leader + hfVilasm + human IgG1Fc							
-----							
Initial Score	=	230	Optimized Score	=	230	Significance	= 2.04
Residue Identity	=	99%	Matches	=	230	Mismatches	= 2
Gaps	=	0	Conservative Substitutions	=	0		
-----							
KLCRDFIMVSOALRLCLLLGLQCLAGGVAKAGSGGTRDMPWPGHPRFVTOEAAHGVLRHRRANAFL							
10	20	30	40	50	60	70	
80	90	100	110	120	130	140	
EELRPGSLERECKERQCSFEAREIFKDAERTKLFWISYDGDQPCASSPCQNGSKDQLQSYICFLPAFE							
150	160	170	180	190	200	210	
GRNCETHKDDQLICVNWNGGCEQYCSHDTGTRKRSRCRHEGYSLLDAGVSCFTPTVYPCGKIPILEKRNASKP							
220	230	240	250	260	270	280	
OGRIVGGKVCPKGECPMQVLLVNGAQLCGGTLINTIWWVSAACHCFDKIKWRNLIAVLGEHDLSEHDGDEQ							
290	300	310	320	330	340	350	
SRRAVQIIPSTVYPTGTTNHDIALRLHQPVLVTHVPLCLPRTFSTERTLAFFRVFSLVSGWGLDRGAT							
370	380	390	400	410	420	430	
ALELMVLNVPRLMTQDCLQSKRKVGDSFNITEYMFCAGYSDGSKDSCAGDSGGPHATYRGTTWLTGIVSWG							
440	450	460	470	480	490	500	
QGCAATVGHFVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFGSAEPKSCDKTHTCTPCPAPPELLGSPSVFLF							
510	520	530	540	550	560	570	
-----							
30	40	50	60	70	80	90	100
PPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEHNAKTKPREQYNSTYRVVSVLTVLHQDWLNL							
110	120	130	140	150	160	170	
PPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEHNAKTKPREQYNSTYRVVSVLTVLHQDWLNL							
510	520	530	540	550	560	570	
-----							
GKEYKCVSNKALPAPIETKISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQP							

|||||  
GKEYCKVSNKALPAPIEKTISKAKGQPREXQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGGP  
580 590 600 610 620 630 640

180 190 200 210 220 230 X  
ENNYKTPPVLDSGSEFLYSKLTVDKSRWQGNVFCVSMHEALHNYTKSLSPGK  
|||||  
ENNYKTPPVLDSGSEFLYSKLTVDKSRWQGNVFCVSMHEALHNYTKSLSPGKXAA  
650 660 670 680 690 700 710

2. US-10-617-619-7 (1-232)  
US-10-030-203-12

Initial Score = 7 Optimized Score = 34 Significance = -0.39  
Residue Identity = 19% Matches = 46 Mismatches = 140  
Gaps = 46 Conservative Substitutions = 0

ALQRPHGLPGFQAPLPSAWASGLPGCRRGRKGLRRNTGHAVEAGASQSLRNPGGSPRRPAPAPARQVRPG  
10 20 30 40 50 60 70

GAAAGLPGEVGQGANVLRGPGDLQGRGEDEAVLDFLOXWGPVCLKMPDWGLLQGPAPVLYLLPPCLRG  
80 90 100 110 120 130 140

PELXDAQXPADLCERERRLXAVLQXPHGHQALLSVPRGVLISAGRRGVLTHTSXISMWNKTYSRKKKQQTP  
150 160 170 180 190 200 210

RPNCGGQVPGRGVSMAGPVVGEVSSVWGDQDHLGLGLRGPIFRQNGELBEEDRGAGRAPRRRGXAE  
220 230 240 250 260 270 280

PAGGAGHHQHVRRPGHHQPHRAAPPAPARGPHXPCGAPLPARTDVLXEDAGLRALLIGORLGPAAAGPWRHG  
290 300 310 320 330 340 350 360

PGAHGAQAPADDPLPAAVTEGGRLPKYHGVHVLCRLHGWQGLLRGGQWRPCHPLPGHVDPGHRQLGP  
370 380 390 400 410 420 430

GLRNRGPIWGVHQGLPVRHVAAKAHALRATPRSPASPISRIRRAQLXQNSHMTVPSTYTPGGTVSLPLP  
440 450 460 470 480 490 500 X  
E

PKSCDKTHTCPCPAPELPGGSVFLFPKPKDTLMISRTPEVTC---VVVDVSHEDPEVKFNWYVDGVEV  
10 20 30 40 50 60  
PKTQGHPI-DLPDPXGHRGG-GREPRPXQVQLVRRGKQXCDKAAGAVQOHVP-----CGQRP  
510 520 530 540 550 560

70 80 90 100 110 120 130  
HNAKTKPREQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKKA-----LPAPIEKTIISKAKGQPREPQVY  
|  
HRPAPGLAEWQ-----GVQV-OGLQSPSPPHRENHLOSQAAPRTTCGVHPAPIPGXADQEPQDPLPGQR  
570 580 590 600 610 620 630

TL-----PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL-DSGSEFLYSKL  
140 150 160 170 180 190  
LLSQHRHRCVGEQWAGQLODHSRAGRLRLLLPQQQ-----HRGQGVQVAGGERLLMLRAXGS---AQPL  
640 650 660 670 680 690

200 X 220 230  
TVDKSRWQGNVFCVSMHEALHNYTKSLSPGK  
HAEPLPVSGXWISG  
700 710

3. US-10-617-619-7 (1-232)  
US-10-030-203-12

Initial Score = 6 Optimized Score = 32 Significance = -0.40

Residue Identity = 19% Matches = 45 Mismatches = 143  
Gaps = 45 Conservative Substitutions = 0

SFAELSSWSPRPSGSSAFCLGFRAAQLQAGSLRPEQEEKGTCRSGRLTSSXPRRKPTASCTCAGAPTRSM  
10 20 30 40 50 60 70

RSCGRAPWRGSARRSAPRRPGRSSRRRGRSCGFLTVMGTSVPQVHARMGAPARTSSPISASASLPBR  
80 90 100 110 120 130 140

AGTVRRTRMTSXSVKTRTAAVSTAVTTTRAPSAPVGATRGTLQWOTGCPAHPOLNIHVEKLYFKXKEMPANP  
150 160 170 180 190 200 210

KAELWGARCAPKGSVHGRSCCWMELSCVGGXPSTPGWSPRPTVSTKSGTYSRCWASTTSASTTGMGR  
220 230 240 250 260 270 280

AGWRRSSSPARTSRAPPTTISRCSACTSPWSSLTWPCSNRSLRGRWPSCASHWAAGASCWTVAPR  
290 300 310 320 330 340 350 360

PWSSWCSTCFQXXPRTACSSHGRWETPQISRSTCSVPATRMAARTPARGTVEAHMPTTGARGTYXRASSAGA  
370 380 390 400 410 420 430

X 10  
EPKSCDKTHTC

RAAQWATLGCPTGSPSTSGCKSSCAQSHAQESSCEPHFPDPQSPNLVTKLTHAHRQAHLNSWGDQSSSS  
440 450 460 470 480 490 X 500

PPCP-ABELLGGP--SVFLFPKPKDTLMISRTPEVT---CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKR  
20 30 40 50 60 70

PQNPRTFSXSPGLRSHAWMTXATKTLRSSSTGTWTAWRCIXPRQS-----RGRSTTARTVWSA--SSPS  
510 520 530 540 550 560

80 90 100 110 120  
BEQVNSTYRVVS--VLTVLHQDWLNGKEYKCKVS-----NKAIPAPIEKTIISKAKGQP

CTRTGXMARSTARSPTKQPPSPKPSKPGSPENXRCTCPHPGMSXPRTRSAKPA-----WSKASIPA  
570 580 590 600 610 620 630

130 140 150 160 170 180 190  
REPQVYTLPSRDELTKNQVSLTCLVKGFYPSDIA-VEWESNGQPENNYKTTTP--PVLDSGSEFLYS-KLT

TSPWSGRAMGSR--RTTTRPLPCWTFPTAPSSSTASSPWTTRAGSRTSSHAPXCMRLCTTTTTRRRRSPCLR  
640 650 660 670 680 690 700

200 X 210 220 230  
VDKSRWQGNVFCVSMHEALHNYTKSLSPGK  
VNDKRP  
710 X

4. US-10-617-619-7 (1-232)  
US-10-030-203-12

Initial Score = 5 Optimized Score = 7 Significance = -0.41  
Residue Identity = 16% Matches = 7 Mismatches = 35  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60 70  
EPKSCDKTHTCPCPAPELPGGSVFLFPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNA

80 90 100 110 120 130 140  
KTKPREQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL

150 160 170 180 190 200 210  
KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSEFLYSKLTVDKSRWQGNVFCVSMHEA

GRLSFTRRQGEALLRVVVVQSLMHG  
X 10 20

220 230 X

LHNHYTKSLSPGK  
AXEDVPLLPALVHGLAVEBEGAVGVQHRGLVVLRLPIALPLHGDVAGIEAFDAQADLVLGOLIPG  
30 40 X 50 60 70 80 90  
WQGVHLXPSGLPFGDGLDGGWEGFVGLDALVLLAIQVVLQDGEDADHTYRAVLLPLRLCLGNMHLH  
100 110 120 130 140 150 160 170  
AVHPVELDLRVFAVHHHACDLRPGPDHGVLFWGEEDXRSQBFRCWARWACVSVTRFGLCGSGKW  
180 190 200 210 220 230 240  
GSQEDSMALXAHELLQPLDVLGDPGVHPKVAHGAALAPADDAPOVPRAPVVGWMASTVPRAGVLAIRV  
250 260 270 280 290 300 310  
AGTEHVLADINGVSHLPXLLQAVLGHQPGHVEHLEQGRGATVQQLAPADQXEAHQORFLRERPFQABG  
320 330 340 350 360 370 380  
HMYSEDHGLVQAEQDQVVVGARDVRAGDDDLRHPALLIPVVLAEVVLQAHRDOVPPVLDVETVGRGDH  
390 400 410 420 430 440 450  
PDGVDQSPPTOLSSIHOOQLPFWLTPFGAHLAPHNSALGFGISFFXNRYFSTWIFNCGCAGHPVCQORVPL  
460 470 480 490 500 510 520 530  
VAPTALGARVVTAVLTAALVHTDOLVILVRLTVPALEGREAEADIGLELVLAGAPILANTXGTLVPIV  
540 550 560 570 580 590 600  
RNPEQLRPLRVLEDPLGLEGALLLALPLQAGRPQLQERVAPAPVQDVGFIILGYEDSVRPLRPHVPC  
610 620 630 640 650 660 670  
PSSXGLSDPACSAALKPKQAEPEGLGDHDEISAK  
680 690 700 710

5. US-10-617-619-7 (1-232)  
US-10-030-203-12

Initial Score = 5 Optimized Score = 37 Significance = -0.41  
Residue Identity = 19% Matches = 54 Mismatches = 146  
Gaps = 71 Conservative Substitutions = 0

RPLIYPETGRGSCNACGAPPHASRRSRRSPANTCSPXACCRGRSRRSPAREAWSCSGSPAACHST  
10 20 30 40 50 60 70  
PRRCRWDRSLXPGSGXPGSWSAHPGAGCTPVVLGAALMLWRFSRWGLGCLWRPCTCTPCHSAPGAG  
80 90 100 110 120 130 140  
RXGRXPHGTCCTAPPALSNXYAPRRPRTSXTXPGILRGSRRPPRXXPKQSGSRXGCPWVLGGRGLTVP  
150 160 170 180 190 200 210  
PGVQVLGTVMCEFCCHKIWARIREMGLAGLGLVALSAXAFATRCTGRPWCTPQSGPRLRSPGSPXRCP  
220 230 240 250 260 270 280  
GTTCPGSHVHLCHPRLRSPCCPSHRRHCTPYLGLSLPPSVTAAGSPGSSAGARXAPXAPGWHRGPAA  
290 300 310 320 330 340 350 360  
GPSRXPMRSARRPASSORTSVRAGRAGPHGQXPRAGAGAACRGWPCGRTCWGXXPAPPAGSAHPRRAR  
370 380 390 400 410 420 430

X  
EPKS-----CDKTHTCPAPPELLGGPSVFLF  
10 20  
XGRAPAPRSGSSXFCRNSGRRPRPRXCSGSPHTLHSPPTGPMADTPLMGTPCPQPGGLGCVWHFFF  
440 450 460 470 480 490 500  
-----PPKPKDTLMTSRTP-----EVTGVVVDVSHEDPEVKFNWYDGVFNHNAKTKPREEQYNSTVRVVSILT  
30 40 50 60 70 80 90  
LEXVFFHMDIQLWVCRTPLRPAESTPRGTDRSAMCF-----CCHCSHAHSR-----RSRSHRS  
510 520 530 540 550  
VLH--QDWLNGKEYCKVKS---NKALP--AP-----IEKTSKAKGQPREPQVYTLPPESR---DE  
100 110 120 130 140

AGHCASHSSGPRRQGRSRVTRTGAQCRSPHSGMDLRHTGPHHCKKSRRTASSSPR--PXRSPGPPRRSTAPP  
560 570 580 590 600 610 620  
LTKQVSLTCLVKGFYPSDIAVESNGQP-----ENNYKTTTPVLDSGSGFFLYSKLTVDKSRWQGNVF  
150 160 170 180 190 200  
CTPSFGPAAAPPGRWRAGAGARRGLPGLRLRCEAPASTACPV-----FL--LLRPARPLRQGSPE  
630 640 650 660 670 680 690  
210 220 230  
SCSVMEALHNHYTKSLSPGK  
700 710 X  
QAEGRGAXGPRPXXNLCKA

6. US-10-617-619-7 (1-232)  
US-10-030-203-12

Initial Score = 5 Optimized Score = 40 Significance = -0.41  
Residue Identity = 21% Matches = 57 Mismatches = 145  
Gaps = 68 Conservative Substitutions = 0

AAAYHLPGDRERLFCVWLCRASCITEHEKTFPCCHLLSTVSLLRKKEPSESSTGGVVLXLFSGCPLLH  
10 20 30 40 50 60 70  
STAMSLGXKPLTRVRLTWFLVSSSRDGRVYTCXSGCPLALEMVFMSGAGRALLETLLHLYSLPFSOSWCR  
80 90 100 110 120 130 140  
TVRLTTRYVLLYCSSRGFLVAXCTSTPSTYQLNLTSGLSSWLTSTTHVTGVRIMRVLSGFGKRKTGDP  
150 160 170 180 190 200 210  
PRSGAGHGHHVXVLSQDLGADPGNGARRRTPGRGSRMSFCSHSMYWTETLVYTPKWPTVAQWPQLTMPV  
220 230 240 250 260 270 280  
RYHVPKXWACGPPPLSPAQESLPSXPAQNMYSVIFGESPTFRDCCRQSWISRGTLSTSSRAVAPRSS  
290 300 310 320 330 340 350 360  
WPQLTNEKRTKASVLSNVRSGRQRTTWSVRTGWCRRSSAMSLVPGTYVLGMMTCATRRRLCSSPSCS  
370 380 390 400 410 420 430  
X  
EPKSCDKTHTCP-----PCPAPELLGGPSVF  
20  
LFPKP-----KDTLMTS--RTPEVTCVVVDVSHEDPEVKFNWYDGVFNH--AKTKPREEQYNS-----  
30 40 50 60 70 80  
LRSCSPSTAIRFLOFLILSKOWAAETQMV-----LIRVPPHNXAPFTNNRTCHGHSPLIGHT  
440 450 460 470 480  
---TYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL--PPSRDELTKNQVSLT  
90 100 110 120 130 140 150  
LPPTIRPMGLLAFLRSRIGIPFGHYSTVGQDTPFSASREYPS--WHRQERLVPVMSLQYCQPPFFFTQISWS  
490 500 510 520 530 540 550 560  
CL-VKGFYPS-----DIATWENSGQP-----ENNYKTTTPVL--DSGSGFFLYSKLTVDKSRWQGNVPSCSV  
160 170 180 190 200 210  
SLCVSQFRPSKAGRKQKQIXDWSWSLQEPFVHGLEAHWSPSLXEQNSFVLSASL--KISR--ASSKHCSS  
570 580 590 600 610 620  
MHEALHNHYTKSLSPGK  
220 230 X  
LH-----SLSRFGRSSRNALARRRRTTPWASWVTKTLXGPGFHGMSRVSPPEALATPPAARQP  
630 640 650 660 670 680 690  
XSPSRQRSLRAWETMMKSLQS  
700 710

**This Page Blank (uspto)**

IntelliGenetics

# FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file us-10-617-619-8.res made by jdelaval on Tue 15 Feb 105 11:34:34-PST.

Query sequence being compared:	US-10-617-619-8 (1-641)
Number of sequences searched:	6
Number of scores above cutoff:	6

Results of the initial comparison of US-10-617-619-8 (1-641) with:  
File : trans.pep

	100-	50-	0
N			
U			
M			
B			
E			
R			
O			
F			
S			
E			
Q			
U			
E			
N			
C			
E			
S			

  

	100-	50-	0
N			
U			
M			
B			
E			
R			
O			
F			
S			
E			
Q			
U			
E			
N			
C			
E			
S			

  

	100-	50-	0
N			
U			
M			
B			
E			
R			
O			
F			
S			
E			
Q			
U			
E			
N			
C			
E			
S			

  

	100-	50-	0
N			
U			
M			
B			
E			
R			
O			
F			
S			
E			
Q			
U			
E			
N			
C			
E			
S			

  

	100-	50-	0
N			
U			
M			
B			
E			
R			
O			
F			
S			
E			
Q			
U			
E			
N			
C			
E			
S			

  

	100-	50-	0
N			
U			
M			
B			
E			
R			
O			
F			
S			
E			
Q			
U			
E			
N			
C			
E			
S			

  

	100-	50-	0
N			
U			
M			
B			
E			
R			
O			
F			
S			
E			
Q			
U			
E			
N			
C			

## PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	32
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	113	9	257.12

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues:	4270
Number of sequences searched:	6
Number of scores above cutoff:	6

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Score	Opt. Score	Sig.	Frame
1. US-10-030-203-12	Sequence 12, Application from mean	712	638	638	2.04	0	0
2. US-10-030-203-12	Sequence 12, Application from mean	712	11	60	-0.40	0	0
3. US-10-030-203-12	Sequence 12, Application from mean	711	8	59	-0.41	0	0
4. US-10-030-203-12	Sequence 12, Application from mean	712	8	57	-0.41	0	0
5. US-10-030-203-12	Sequence 12, Application from mean	711	7	98	-0.41	0	0
6. US-10-030-203-12	Sequence 12, Application from mean	712	7	42	-0.41	0	0

1. US-10-617-619-8 (1-641)  
US-10-030-203-12 Sequence 12. Application US/10030203

Sequence 12, Application US/10030203

**GENERAL INFORMATION:**

APPLICANT: Alan Garen

APPLICANT: Zhiwei Hu

**TITLE OF INVENTION: Neovascular-Targeted Immunoconjugates**

FILE REFERENCE: OCR-679B.US

CURRENT APPLICATION NUMBER: US/10/030,203

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: PCT/US00/16481

PRIOR FILING DATE: 2000-06-14

NUMBER OF SEQ ID  
SOFTWARE: MS DOG

SOFTWARE: MS DOS  
CFO ID NO 12

SEQ ID NO 12  
LENGTH: 2139

LENGTH: 2138  
TYPE: DNA

TYPE: DNA  
ORGANISM:

ORGANISM: ARTIFICIAL sequence  
FEATURE:

FEATURE: NAME/KEY	DESCRIPTION
1. <b>Product Name</b>	Product Name
2. <b>Product Description</b>	Product Description
3. <b>Product Price</b>	Product Price
4. <b>Product Category</b>	Product Category
5. <b>Product Image</b>	Product Image
6. <b>Product Availability</b>	Product Availability
7. <b>Product Rating</b>	Product Rating
8. <b>Product Reviews</b>	Product Reviews
9. <b>Product Tags</b>	Product Tags
10. <b>Product Meta Data</b>	Product Meta Data
11. <b>Product SEO</b>	Product SEO
12. <b>Product Analytics</b>	Product Analytics
13. <b>Product Security</b>	Product Security
14. <b>Product Performance</b>	Product Performance
15. <b>Product Support</b>	Product Support
16. <b>Product Training</b>	Product Training
17. <b>Product Documentation</b>	Product Documentation
18. <b>Product Feedback</b>	Product Feedback
19. <b>Product Updates</b>	Product Updates
20. <b>Product Version</b>	Product Version
21. <b>Product License</b>	Product License
22. <b>Product Warranty</b>	Product Warranty
23. <b>Product Return Policy</b>	Product Return Policy
24. <b>Product Shipping Policy</b>	Product Shipping Policy
25. <b>Product Payment Policy</b>	Product Payment Policy
26. <b>Product Privacy Policy</b>	Product Privacy Policy
27. <b>Product Terms of Service</b>	Product Terms of Service
28. <b>Product Disclaimer</b>	Product Disclaimer
29. <b>Product Copyright</b>	Product Copyright
30. <b>Product Trademark</b>	Product Trademark
31. <b>Product Patent</b>	Product Patent
32. <b>Product Design</b>	Product Design
33. <b>Product Development</b>	Product Development
34. <b>Product Testing</b>	Product Testing
35. <b>Product Deployment</b>	Product Deployment
36. <b>Product Maintenance</b>	Product Maintenance
37. <b>Product Support</b>	Product Support
38. <b>Product Training</b>	Product Training
39. <b>Product Documentation</b>	Product Documentation
40. <b>Product Feedback</b>	Product Feedback
41. <b>Product Updates</b>	Product Updates
42. <b>Product Version</b>	Product Version
43. <b>Product License</b>	Product License
44. <b>Product Warranty</b>	Product Warranty
45. <b>Product Return Policy</b>	Product Return Policy
46. <b>Product Shipping Policy</b>	Product Shipping Policy
47. <b>Product Payment Policy</b>	Product Payment Policy
48. <b>Product Privacy Policy</b>	Product Privacy Policy
49. <b>Product Terms of Service</b>	Product Terms of Service
50. <b>Product Disclaimer</b>	Product Disclaimer
51. <b>Product Copyright</b>	Product Copyright
52. <b>Product Trademark</b>	Product Trademark
53. <b>Product Patent</b>	Product Patent
54. <b>Product Design</b>	Product Design
55. <b>Product Development</b>	Product Development
56. <b>Product Testing</b>	Product Testing
57. <b>Product Deployment</b>	Product Deployment
58. <b>Product Maintenance</b>	Product Maintenance
59. <b>Product Support</b>	Product Support
60. <b>Product Training</b>	Product Training
61. <b>Product Documentation</b>	Product Documentation
62. <b>Product Feedback</b>	Product Feedback
63. <b>Product Updates</b>	Product Updates
64. <b>Product Version</b>	Product Version
65. <b>Product License</b>	Product License
66. <b>Product Warranty</b>	Product Warranty
67. <b>Product Return Policy</b>	Product Return Policy
68. <b>Product Shipping Policy</b>	Product Shipping Policy
69. <b>Product Payment Policy</b>	Product Payment Policy
70. <b>Product Privacy Policy</b>	Product Privacy Policy
71. <b>Product Terms of Service</b>	Product Terms of Service
72. <b>Product Disclaimer</b>	Product Disclaimer
73. <b>Product Copyright</b>	Product Copyright
74. <b>Product Trademark</b>	Product Trademark
75. <b>Product Patent</b>	Product Patent
76. <b>Product Design</b>	Product Design
77. <b>Product Development</b>	Product Development
78. <b>Product Testing</b>	Product Testing
79. <b>Product Deployment</b>	Product Deployment
80. <b>Product Maintenance</b>	Product Maintenance
81. <b>Product Support</b>	Product Support
82. <b>Product Training</b>	Product Training
83. <b>Product Documentation</b>	Product Documentation
84. <b>Product Feedback</b>	Product Feedback
85. <b>Product Updates</b>	Product Updates
86. <b>Product Version</b>	Product Version
87. <b>Product License</b>	Product License
88. <b>Product Warranty</b>	Product Warranty
89. <b>Product Return Policy</b>	Product Return Policy
90. <b>Product Shipping Policy</b>	Product Shipping Policy
91. <b>Product Payment Policy</b>	Product Payment Policy
92. <b>Product Privacy Policy</b>	Product Privacy Policy
93. <b>Product Terms of Service</b>	Product Terms of Service
94. <b>Product Disclaimer</b>	Product Disclaimer
95. <b>Product Copyright</b>	Product Copyright
96. <b>Product Trademark</b>	Product Trademark
97. <b>Product Patent</b>	Product Patent
98. <b>Product Design</b>	Product Design
99. <b>Product Development</b>	Product Development
100. <b>Product Testing</b>	Product Testing
101. <b>Product Deployment</b>	Product Deployment
102. <b>Product Maintenance</b>	Product Maintenance
103. <b>Product Support</b>	Product Support
104. <b>Product Training</b>	Product Training
105. <b>Product Documentation</b>	Product Documentation
106. <b>Product Feedback</b>	Product Feedback
107. <b>Product Updates</b>	Product Updates
108. <b>Product Version</b>	Product Version
109. <b>Product License</b>	Product License
110. <b>Product Warranty</b>	Product Warranty
111. <b>Product Return Policy</b>	Product Return Policy
112. <b>Product Shipping Policy</b>	Product Shipping Policy
113. <b>Product Payment Policy</b>	Product Payment Policy
114. <b>Product Privacy Policy</b>	Product Privacy Policy
115. <b>Product Terms of Service</b>	Product Terms of Service
116. <b>Product Disclaimer</b>	Product Disclaimer
117. <b>Product Copyright</b>	Product Copyright
118. <b>Product Trademark</b>	Product Trademark
119. <b>Product Patent</b>	Product Patent
120. <b>Product Design</b>	Product Design
121. <b>Product Development</b>	Product Development
122. <b>Product Testing</b>	Product Testing
123. <b>Product Deployment</b>	Product Deployment
124. <b>Product Maintenance</b>	Product Maintenance
125. <b>Product Support</b>	Product Support
126. <b>Product Training</b>	Product Training
127. <b>Product Documentation</b>	Product Documentation
128. <b>Product Feedback</b>	Product Feedback</

NAME/KEY: CDS  
OTHER INFORMATION:

OTHER INFORMATION: includes leader + hfvilla

# STREET NUMBER + HOUSE NUMBER : NOTED JOINT WEIRDO

```
Initial Score      = 638  Optimized Score = 638  Significance = 2.04
Residue Identity = 97%  Matches      = 628  Mismatches = 13
Gaps              = 0    Conservative Substitutions = 0
```

KLCDFFIMYSQALRLCLLGLQGLAAGGVAKAGCGGCTEDPMWKPGRFVFVQBEAHGVLHRRRRANAFL  
10 20 30 40 50 60 70  
X ANAFL  
|||

10 20 30 40 50 60 70  
XXLRPGSLRXCKXXQCXXFXRXIFKDXRTKLFWSYSDGDCASSPQNGSKNDQSQSYICFLCPAPE  
BEURPGSLERECKEQCSFEAREIFKDAERTKLFWSYSDGDCASSPQNGSKNDQSQSYICFLCPAPE

GRNCETHKDDQLICVNEGGEQYCSDHGTGKSRCHGEGYSLADGVSCTPTVEYPCGKIPILEKRNASKP  
GRNCETHKDDQLICVNEGGEQYCSDHGTGKSRCHGEGYSLADGVSCTPTVEYPCGKIPILEKRNASKP  
GRNCETHKDDQLICVNEGGEQYCSDHGTGKSRCHGEGYSLADGVSCTPTVEYPCGKIPILEKRNASKP  
GRNCETHKDDQLICVNEGGEQYCSDHGTGKSRCHGEGYSLADGVSCTPTVEYPCGKIPILEKRNASKP  
GRNCETHKDDQLICVNEGGEQYCSDHGTGKSRCHGEGYSLADGVSCTPTVEYPCGKIPILEKRNASKP

0 160 170 180 190 200 210 220  
 QGRIVGGKVPKGECPWQLLVNQAQLCGTGLINTWVYSAACFDKIKNWRNLIAVGEHDLSEHDGDEQ  
 QGRIVGGKVPKGECPWQLLVNQAQLCGTGLINTWVYSAACFDKIKNWRNLIAVGEHDLSEHDGDEQ  
 QGRIVGGKVPKGECPWQLLVNQAQLCGTGLINTWVYSAACFDKIKNWRNLIAVGEHDLSEHDGDEQ  
 QGRIVGGKVPKGECPWQLLVNQAQLCGTGLINTWVYSAACFDKIKNWRNLIAVGEHDLSEHDGDEQ

SRRAQVIIPSTTYVEGTTHDIALRLHQPVVLTDHVVPICLPERTSERTLAFVRFSLVSGHQLLDRGAT  
SRRAQVIIPSTTYVEGTTHDIALRLHQPVVLTDHVVPICLPERTSERTLAFVRFSLVSGHQLLDRGAT  
SRRAQVIIPSTTYVEGTTHDIALRLHQPVVLTDHVVPICLPERTSERTLAFVRFSLVSGHQLLDRGAT  
SRRAQVIIPSTTYVEGTTHDIALRLHQPVVLTDHVVPICLPERTSERTLAFVRFSLVSGHQLLDRGAT

300 310 320 330 340 350 360  
ALELMVLNVPRLMTQDCLOQSRKVGDSPNITEYMFCAVSDGSKDCKGSGGPHATHYRGTWLTGIVSWG

```
|||||370380390400410420430|||||
ALELMLNVPRLMTQDCLQSKRGVDSNITEYMFACGSDGSCAGDSGGPHATHYRGTWYLTGLIVSWG
370380390400410420430
QGCAVGHFVYRVSYQVIEWLQKLMRSEPRGVLLRAPFGSABPKSCDKTHTCCPCAPAPELLGGPSVFLF
370380390400410420430
QGCAVGHFVYRVSYQVIEWLQKLMRSEPRGVLLRAPFGSABPKSCDKTHTCCPCAPAPELLGGPSVFLF
440450460470480490500
PPKPKDTLM:SRTEPVTVCVVDVSHEDPEVFNKYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
PPKPKDTLM:SRTEPVTVCVVDVSHEDPEVFNKYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
510520530540550560570
GKEYKCKVSNKALPAPIEKTISKAKGQPREQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
580590600610620630640
GKEYKCKVSNKALPAPIEKTISKAKGQPREQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
590600610620630640X
ENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSLSPGK
ENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSLSPGKXAA
650660670680690700710
```

2. US-10-617-619-8 (1-641)  
US-10-030-203-12

Initial Score = 11 Optimized Score = 60 Significance = -0.40  
Residue Identity = 17% Matches = 77 Mismatches = 299  
Gaps = 72 Conservative Substitutions = 0

```
ANAFLLXLRPGSLXRCXKXQCSFXAXRIFKDAKXTKLFWISYSDGQDQACSSPCQNGSKDQIQSYICPC
8090100110120130140
LPAFEGRCNETHKDDQLICVNNEGCGEYCDSDHTGTRKRCRCHGYSLLADGVSCPTPTVEYPCGKIPILEKR
150160170180190200210
NASRPGQIRGVGKVCPCGCEPWQVLLVNGAQLCGGTLINTIWWVSAHCFDKIKNENLTVLAGEHDLSEH
220230240250260270280
DGDSQSRRAVQIIIPSTYVPGTTHDIALLLHLPVWLTDHVPLCLPRTFSBRTLA--FVRFSLVSGWGQ
RPLIITYPTGRGSSACSCAEP--HASRSMRRSSPAATCSCPXACCGRSRRS---
X1020304050
290300310320330340350
LLDRGA----TALMLVNLVRLMTQDCLQSKRGVDSNITEYMFACGSDGSKDQSGGPHATHYRG
-PAREAWSCSGPAHCSPTPRCRWD---RSLXPGRSXPGSWSAHPGAGCTPVVLGAALMLWRWFSR-
60708090100110120
TWYLTG-----IVSWGQCATVGHFG--VYTRVSYQVIEWLQKLMRSEPRGVLLRAPFGSABPK
360370380390400410
-WLGLGLCWRRPCTCTPCHSAGSPGAGRGXPHGTCCCTAPPAALSWXYAPPR-RPRTSXTXPOGLGRSRPPP
130140150160170180190
420430440450460470480
SCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTVCVVDVSHEDPEVFNKYVDGVEVHNAKT-
|||||
RMXPQSGRSXGCPWVLGGRLATVPPGVQVLTGVMCEFCFKIWKALRIEMGLAGLGLGVALSAXAFAPAR
200210220230240250260
-----KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRBPQVYT
490500510520530540
```

```
CTGRPWCTQSGPRLRPGSPXRCPSCGTTTCFSGWHVGLHCPRRSPCCHP-----SSRHRTCTPYXLGS
270280290300310320
LPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR-----WQ
|||||
LPPSVTAAGSPGSS-----AGARXAPXAPGFWRHG-PAAGPSRXP--MRSAARRPASSQRTSVRAGRAPHQ
330340350360370380390
620630640
QGNVFCSCVMHEALHNNHYTKSLSLSPGK
XG-----PRAGAGAAARCRGWPCGRTCGWXXPAPPAGSAHPRARXGRAPAPRSPSSSXXFCRNSGP
400410X420430440450
RPPRCXSGSPHTTELHSTPTTGPMADTPLNGTFCPPQFGVLGVCMWHFFFLXVFFHMDIQLWVCRTPLPAE
460470480490500510520
STPRGTDRSACWPCGCHGCHTAHSRRSRSHRSAGHPCASHSGPRRQGGRSRYRTGAGFCRSPHSGMDLHRTGP
530540550560570580590
HHCKKSTASSPRPXSPGPPRRSTAPPCTPSPGSAAPPGTTRWAGACAGRRGLPPGLRLCEAPASTA
600610620630640650660670
CPVFLLRXPXPRLPQGPSPEAQAEGRGAXGFGREXXNLCKA
680690700710
```

3. US-10-617-619-8 (1-641)  
US-10-030-203-12

Initial Score = 8 Optimized Score = 39 Significance = -0.41  
Residue Identity = 21% Matches = 53 Mismatches = 149  
Gaps = 50 Conservative Substitutions = 0

```
GRLSFTRRQGEALLRVVVVQSLMHGHGAXEDVPLPALVHGELAVEEGAVGVQHGRRGLVVLRLPTALPL
10203040506070
HGDVAGIEAFDOAGQADVLGLQLIPGNGQGVHLXFSGLPFGDGLDGGWEGFVGLDALVLLAIQPLVQD
8090100110120130140
GEDADHTVRAVLLLPRLCLGXMHLMHVAHVFPVELDLRVFVAHVHHACDLRPGDGHGVLGFWGSEEDXRSP
150160170180190200210
QEFRCWAWACVSFVTRFGLCGSKGWSQEDSWAHLXAHELLOPLDLVLDGDPGVHPKVAHGAALAPADDAQ
220230240250260270280
VPRAPVVVGWMASTVPRAGVLAIRVAGTEHVLRIWGVSHLPXLLQAVLGHQPGHVEHHELOGRGATVQQL
290300310320330340350360
APAAOXYEAHEGQRPBERPFGQAEHHMVSEDHGLVQAEQRDVVVGARDVRAGDDDLRHPALLIPVILA
370380390400410420430
EVVLAHQRDQVPPVLDVETVGRGDHPDGVDPQPTQLSSITHQQDLPLPWLTPFGAHLAP--HNSALGPAQIS
440450460470480X490500
FXXAR-----XIF-----KDAKRTKLFMISYSDG--DQCASSPCQNGSKDQLOSICYCLPAPFGRNC
304050607080
FFXNRPSTWIFNCGCAGHPVCQQRVPLVAPTALGALGARVVTAVLLTAALVHTTQVLTVLRLTVPALEGRE
510520530540550560570
ETHKDDQL-----ICVNNEGCGEYCDHTGTRKRCRCHGYSLLADGVSCPTPTVEYPCGKIPII--EKRN
90100110120130140
EADIGLELVLAGAPILAWTGTLPITVRNPEQLRPLRVLEDLPGLLG-ALLLLALPLQGARQLQERVG
580590600610620630640
150160170180190200210
```





390 400 410 420 430 440  
-----QYIEWLQKMRSEPPGVLRLRAPPPGSAEPKSCDKTHTCP---PCPAPPELLGGPSVFLFPKPKDT  
PPASPIRIIRAQILXONSHMPTVPSTXTPGTVSLPLPKTKQCHPHDLDPKXHMGG-GRPRRRXGQVQ  
470 480 490 500 510 520 530  
450 460 470 480 490 500 510  
LMISRTPEVTC---VVVDVSHDEPEVKFNWYDGVVHNAKTPREEQYNSTYRVVSVLTVLHODWNGKE  
LVRRRGACQODKAAGAVQOQHP-----CGQRPHPAPGLAEWQ-----GVQV-OGLOQSPSPHR  
540 550 560 570 580 590  
520 530 540 550 560  
YKCKVSNKA-----LPAPTEKTSKAKGQPREPPQVVTL-----PPSRDELTKQVSLTCLVKGY  
ENHLOSQAAPRTTGVPAPIPGKADQEPGQDPLPGQRLLSQRHRRGVGEWAAGEQLQDHASRAGLRLLL  
600 610 620 630 640 650 660  
570 580 590 600 610 X 630  
PSDIAVWESNGQPENNYKTTTPVL-DSDGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSL  
PLOQA-----HRQEQVAGERLLMLRAXGS---AQPLHAEPLPVSGXMI  
670 680 690 700 710  
640  
PGK

6. US-10-617-619-8 (1-641)  
US-10-030-203-12

Initial Score = 7 Optimized Score = 42 Significance = -0.41  
Residue Identity = 19% Matches = 62 Mismatches = 187  
Gaps = 70 Conservative Substitutions = 0

SFAEISWSPPRGSSAFCLGFRAAWLQAGSLRPQEEKHGTCRSGLTSSXPRRKPTASCTGAGAPTRSW  
10 20 30 40 50 60 70  
80 90 100 110 120 130 140  
RSCGRAPWRGARRSSAPRRPGRSSRTRGRSCGFLTVMGTSVPQVHARMGAPARTSSSPIASASLPSR  
AGTVRRTRMTSXVXKTRTAAVSTAVTTTRAPAPVATRGTLQWTCGPAHPQNLNIVHEKYLFXKEMPAMP  
150 160 170 180 190 200 210  
KAEIWAARCAPKGVHGRSCCWXNELSCVGPXSTPSCWSRPRVTYSKRTGGTXSRCAWSTTTSASTGMGR  
220 230 240 250 260 270 280  
AGWRRSSSPARTSRAPPTTTSRCASCTSPWSSLTMCPSACPNGRSLRGRWPSCASHWSAAGASCWTVAPR  
290 300 310 320 330 340 350 360  
PWSSWCSTCPGXPRTACSSHGRMETPQISRSTCSVPATRMAARTPARGTVEAHMPPTTGARGTXRASSAGA  
370 380 390 400 410 420 430  
X 10 20 30 40 50  
ANAPFLXLRPG---SLXRXCKXQCSFXXA-----RXIFKD-----AXRTKLFWISYSDGDCASSPCON  
RAAQFWATL-CCTFGSPSTSGCK-SSCAQSHAQESSCEPHFPQSPNLVTKL---THAHRAOHLNSWGDR  
440 450 460 470 480 490  
60 70 80 90 100 110 120  
GGSCKDQ-LQSVICFLPAFEGRNCEHDKDQILCVNENGGEQVCSDDHTGKRSRC-HEGYS-LIA  
QSSSSPQNPRTPFSKSPGLRSHAWWTATKTL-----RSSSTGTWTAWRCIXPRQSRGRSSTTA  
500 510 520 530 540 550  
DGV-----SCTVVEYPCGKIPILEKRNASKPQRIVGGKVCPRGECQWQVLLLVNGAQLCGGTLINTIWW  
RTVWSASSPSCTRT-GXWARTSARSPTKQPPSRKPSK-PKG-----SPENXRCTPCPHPGMSXPRT---  
560 570 580 590 600 610 620  
190 200 210 220 230 240 250

VSAACHCFDKIKNWRNLIAVLGEHDLSEHDG-DEQSRRAQVVIIPSTVYVPGTTNHDIA--LLRLHQPVLVTDH  
RSAXPAWSK-----ASIPATSPWSGRAMGSRRTTTRPRLPCWMTPTAPSSSTASSPWTRAGSGRTSS  
630 640 650 660 670 680  
260 270 280 290 X 300 310 320  
VVPLCLPRTFSRTTAFVRFSLVSGWQLDRGATALELMVLNVPRLMTQDCLQOSRKVGDSPNITEYMF  
HAPXCMELCTTTTTRRA-----SPCLRVDNDRP  
690 700 710 X  
330 340 350 360 370 380 390 400  
AGYSDGSKDSCKGDSGGPHATHYRGTYLTGIVSWGQCATVGHFYTRVSVQVIEWLQKLMRSEPRPGVLL  
410 420 430 440 450 460 470  
RAPPPGSAEPKSCDKTHTCPCPAPPELLGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNMYV  
480 490 500 510 520 530 540  
DGYEVHNAKTKPREEQYNSTYRVSVLTVLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL  
550 560 570 580 590 600 610  
PPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSGDSFELYSKLTVDKSRWQGNVF  
620 630 640  
SCSYMHEALHNNHYTKQSLSLSPGK